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~~56.~~ A sequence according to claim ~~53~~, wherein the sequence is derived from a *Triticum* species.

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~~57.~~ A sequence according to claim ~~56~~, wherein the *Triticum* species is *Triticum tauschii*.

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~~58.~~ A sequence according to claim ~~53~~, wherein the sequence encodes starch branching enzyme I or a biologically-active fragment thereof, and wherein the sequence has at least 70% sequence homology with the sequence shown in SEQ ID NO:5 or SEQ ID NO:9.

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~~59.~~ A sequence according to claim ~~58~~, wherein the homology is at least 90%.

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~~60.~~ A sequence according to claim ~~53~~, wherein the sequence encodes starch branching enzyme II a or biologically-active fragment thereof, and wherein the sequence has at least 70% sequence homology with the sequence shown in SEQ ID NO:10.

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~~61.~~ A sequence according to claim ~~60~~, wherein the homology is at least 90%.

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~~62.~~ A sequence according to claim ~~53~~, wherein the sequence encodes soluble starch synthase or a biologically-active fragment thereof, and wherein the sequence has at least 70% sequence homology with the sequence shown in SEQ ID NO:11 or SEQ ID NO:13.

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~~63.~~ A sequence according to claim ~~62~~, wherein the homology is at least 90%.

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~~64.~~ A sequence according to claim ~~63~~, wherein the sequence encodes a 75 kD soluble starch synthase of wheat.

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~~65.~~ A sequence according to claim ~~64~~, which encodes an amino acid sequence at least 70% homologous to that shown in SEQ ID NO:14.

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~~66.~~ A sequence according to claim ~~53~~, wherein the sequence encodes debranching enzyme or a biologically-active fragment thereof, and wherein the sequence has at least 70% sequence homology with the sequence shown in SEQ ID No:17.

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A sequence according to claim 66, wherein the homology is at least 90%.

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68.
A promoter of an enzyme selected from the group consisting of starch branching enzyme I, starch branching enzyme II, starch soluble synthase I, and debranching enzyme, with the proviso that the enzyme is not soluble starch synthase I of rice, or starch branching enzyme I of rice or maize.

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69.
claim 58.
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70.
A nucleic acid construct comprising a nucleic acid sequence according to

A nucleic acid construct for targeting a gene to the endosperm of a cereal plant, comprising one or more promoter sequences according to claim 68, 38, operatively linked to a nucleic acid sequence encoding a protein, wherein the expression of the targetted gene in the endosperm of a cereal plant is modified.

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A method of modifying the characteristics of starch produced by a plant, comprising the steps of:

- (a) introducing a nucleic acid sequence according to claim 1 into a host plant, and/or
- (b) introducing an anti-sense nucleic acid sequence directed to a gene encoding an enzyme of the starch biosynthetic pathway into a host plant, wherein the enzyme is selected from the group consisting of starch branching enzyme I, starch branching enzyme II, starch soluble synthase I, and debranching enzyme, with the proviso that the enzyme is not soluble starch synthase I of rice, or starch branching enzyme I of rice or maize, and wherein if both steps (a) and (b) are used, the enzymes in the two steps are different.

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72.
A method of modulating the time of expression of a gene in endosperm of a cereal plant, comprising the step of transforming the plant with a construct according to claim 68.

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A plant transformed with a construct according to claim 69.